

REMARKS

Claims 1, 2, 4-10, and 12-35 are now pending in the application. Features of former dependent claims 3 and 11 are incorporated into independent claim 1; accordingly, claims 3 and 11 are cancelled. Claims 22-35 are withdrawn. The Examiner is respectfully requested to reconsider and withdraw the rejections in view of the amendments and remarks contained herein.

SPECIFICATION

The specification stands objected to for certain informalities. Applicants have amended the specification according to the Examiner's suggestions. Therefore, reconsideration and withdrawal of this objection are respectfully requested.

REJECTION UNDER 35 U.S.C. § 112

Claims 14-18 stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point and distinctly claim the subject matter which Applicant regards as the invention. This rejection is respectfully traversed.

Claims 14-18 recite the feature "said viewer" in line 2. These claims each depend on claim 13, which also recites "said viewer" in line 2, and where claim 13 is dependent on claim 1. Independent claim 1 introduces "a viewer adapted to integrate the comparative genomic data." Thus, "said viewer" in claims 14-18 each stems from "said viewer" in claim 13, which stems from "a viewer adapted to integrate the comparative genomic data" from claim 1. Claim 13 recites a group of various viewer

components (i.e., viewer components (a) through (f)) and claims 14-18 describe viewers containing various numbers of these viewer components.

As a result, there is sufficient antecedent basis for "said viewer" in claims 14-18 as this feature directly follows from claim 13 which follows from claim 1. Applicants respectfully request reconsideration and withdrawal of the rejection.

REJECTION UNDER 35 U.S.C. § 102

Claims 1-10, 12-17, 19 and 21 stand rejected under 35 U.S.C. § 102(b) as being anticipated by Kent et al. (Genome Research, Vol. 12, pages 996-1006, June, 2002) (hereinafter Kent). This rejection is respectfully traversed.

Amended independent claim 1 includes a viewer adapted to integrate the comparative genomic data, wherein the viewer comprises a multiple sequence alignment viewer which shows multiple sequence alignments of genomic sequences of the at least two species. The multiple sequence alignment viewer is incorporated from former dependent claim 11 that was not anticipated by Kent. In view of the amendment, the present rejection is rendered moot, as the remaining claims all trace their dependency to amended independent claim 1. Applicants respectfully request reconsideration and withdrawal of the rejection.

Claims 1, 3, 4, 8, 9, 10, 13, 15, and 21 stand rejected under 35 U.S.C. § 102(b) as being anticipated by Semple (Genome Research, Vol. 2, pages 2001.1-2001.6, June, 2001) (hereinafter Semple). This rejection is respectfully traversed.

Amended independent claim 1 includes a viewer adapted to integrate the comparative genomic data, wherein the viewer comprises a multiple sequence alignment viewer which shows multiple sequence alignments of genomic sequences of the at least two species. The multiple sequence alignment viewer is incorporated from former dependent claim 11 that was not anticipated by Semple. In view of the amendment, the present rejection is rendered moot, as the remaining claims all trace their dependency to amended independent claim 1. Applicants respectfully request reconsideration and withdrawal of the rejection.

Claims 1-5, 7-20 stand rejected under 35 U.S.C. § 102(3) as being anticipated by Sears et al. (Patent Publication #2003/0220820) with a priority date of November 13th, 2001 (hereinafter Sears). This rejection is respectfully traversed.

Amended independent claim 1 includes an interactive display system including, among other features, a database of comparative genomic data from at least two species, wherein the comparative genomic data comprises syntenic anchors and syntenic blocks from the two or more species. Sears cannot anticipate independent claim 1 as the reference is missing at least two features of the present claim. In particular, Sears does not disclose comparative genomic data comprising syntenic anchors and syntenic blocks. In fact, Sears is completely silent on what syntenic features and/or methods are used to determine orthologous regions.

Claim 1 includes a viewer adapted to integrate comparative genomic data from at least two species where the data includes syntenic anchors and syntenic blocks. Synteny refers to linkage of genes in different species where gene order in

chromosomes may be conserved over wide evolutionary distances. Paragraph [0056]. Syntenic anchors and blocks are two specific features determined from genomic comparison between at least two species. A syntenic anchor refers to conserved locations in two genomes that are identified by significant DNA sequence similarity and constitute a bi-directionally unique match (i.e., two segments can be designated syntenic anchors if their alignment may be the only significant match either segment may be shown to have to the other genome). A syntenic anchor may have different genomic coordinates in each different species in which it may be identified. Paragraph [0057]. A syntenic block refers to evolutionary conserved regions between two species where the majority of syntenic anchors is consistent with each other and is in mostly consecutive order. A syntenic block may have different genomic coordinates in each different species in which it is identified. Paragraph [0058]. Thus, genomic data including the syntenic anchors and blocks includes chromosomal regions that may include the ordering of several genes. Syntenic anchors and blocks are further illustrated in Figure 1 and paragraphs [0025] and [0067]-[0068].

Several different sources of evidence, including SA NUMBER, SA COVERAGE, BLOCK, and PANTHER and GO, can be used to help identify and compare putative orthologs (i.e., two genes of different species that share a common evolutionary ancestry) as shown in Table 1. Paragraphs [0054], [0064]-[0066], and [0069]-[0073]. For example, SA NUMBER and SA COVERAGE depend on the shared syntenic anchors and BLOCK shows whether two orthologous transcripts belong to the same syntenic block. Thus, syntenic anchors and syntenic blocks are specific types of data that can be used in identification of orthologs.

In contrast to claim 1, Sears does not teach syntenic anchors and syntenic blocks in comparison of genomic data from at least two species. In fact, Sears is completely silent as to what data and/or methods are used in determining orthologous (syntenic) regions between mouse and human chromosomes. Sears only discloses data including “orthologous (syntenic) regions” in paragraph [0035] and claims 9 and 10. The apparent disclosure of the genus (i.e., orthologous (syntenic) regions) does not anticipate the species (i.e., syntenic anchors and syntenic blocks), since there is no teaching in Sears as to how orthologous (syntenic) regions are determined or what data or types of data have contributed to their determination. *Metabolite Laboratories, Inc. v. Laboratory Corporation of America Holdings*, 370 F.3d 1354, 71 USPQ2d 1081, 1091 (Fed. Cir. 2004) (A prior art reference that discloses a genus still does not inherently disclose all species within that broad category. See *Corning Glass Works v. Sumitomo Elec. U.S.A., Inc.*, 868 F.2d 1251, 1262 [9 USPQ2d 1962] (Fed. Cir. 1989) (“Under [defendant’s] theory, a claim to a genus would inherently disclose all species. We find [this] argument wholly meritless”)).

In view of the Sears reference failing to teach these two claim features, Applicants respectfully request reconsideration of the claims and withdrawal of the rejection.

CONCLUSION


It is believed that all of the stated grounds of rejection have been properly traversed, accommodated, or rendered moot. Applicant therefore respectfully requests that the Examiner reconsider and withdraw all presently outstanding rejections. It is

believed that a full and complete response has been made to the outstanding Office Action and the present application is in condition for allowance. Thus, prompt and favorable consideration of this amendment is respectfully requested. If the Examiner believes that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (248) 641-1600.

Respectfully submitted,

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